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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=5; day=16; hr=13; min=38; sec=54; ms=436;]

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Reviewer Comments:

<210> 1

<211> 0

<212> PRT

<213> human

<220>

<221> MISC_FEATURE

<222> (0)..(0)

<223> non-contiguous amino acid sequence of D1, D2, D3, and D4 regions of human SMS1

<400> 1

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If the above attachment is a intentionally skipped sequence. The format to be used is as bleow:

<210>1

<400>1

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This type of error is seen in other sequences too.

Application No: 10563744 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-30 21:08:45.665
Finished: 2008-04-30 21:08:48.081
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 416 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
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Input Set:

Output Set:

Started: 2008-04-30 21:08:45.665
Finished: 2008-04-30 21:08:48.081
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 416 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Universiteit Utrecht Holding B.V.
 Holthuis, Josephus Carolus Maria
 Huitema, Klasina Rinsje

<120> Newly Identified Cholinephosphotransferases and
 ethanolaminephosphotransferases

<130> 03-702-A

<140> 10563744
 <141> 2008-04-30

<150> PCT/NL04/00488
 <151> 2004-07-07

<150> EP 030789325
 <151> 2003-12-18

<150> US 60/485202
 <151> 2003-07-07

<160> 22

<170> PatentIn version 3.5

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 <213> human

<220>
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 <223> non-contiguous amino acid sequence of D1, D2, D3, and D4 regions
 of human SMS1

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 <213> human

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 of human SMS2

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<213> C. elegans

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of C. elegans SMS1

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of P. falciparum SMS1

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<213> human

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of human SMSr

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<213> *D. melanogaster*

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<223> non-contiguous amino acid sequence of D1, D2, D3, and D4 regions
of *D. melanogaster* SMSr

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<211> 0
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<213> *C. elegans*

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 of C. elegans SMSr

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 of C. elegans SMSdr

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Leu Glu Asn Ala Met Pro Glu Tyr Cys Glu Pro Leu Glu His Phe Thr
 20 25 30

Gly Gln Asp Leu Ile Asn Leu Thr Gln Glu Asp Phe Lys Lys Pro Pro
 35 40 45

Leu Cys Arg Val Ser Ser Asp Asn Gly Gln Arg Leu Leu Asp Met Ile
 50 55 60

Glu Thr Leu Lys Met Glu His His Leu Glu Ala His Lys Asn Gly His
 65 70 75 80

Ala Asn Gly His Leu Asn Ile Gly Val Asp Ile Pro Thr Pro Asp Gly
 85 90 95

Ser Phe Ser Ile Lys Ile Lys Pro Asn Gly Met Pro Asn Gly Tyr Arg
 100 105 110

Lys Glu Met Ile Lys Ile Pro Met Pro Glu Leu Glu Arg Ser Gln Tyr
115 120 125

Pro Met Glu Trp Gly Lys Thr Phe Leu Ala Phe Leu Tyr Ala Leu Ser
130 135 140

Cys Phe Val Leu Thr Thr Val Met Ile Ser Val Val His Glu Arg Val
145 150 155 160

Pro Pro Lys Glu Val Gln Pro Pro Leu Pro Asp Thr Phe Phe Asp His
165 170 175

Phe Asn Arg Val Gln Trp Ala Phe Ser Ile Cys Glu Ile Asn Gly Met
180 185 190

Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr Lys
195 200 205

Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr Leu
210 215 220

Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly Met
225 230 235 240

His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln Leu
245 250 255

Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr Gly
260 265 270

Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val Met
275 280 285

Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg Leu
290 295 300

Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile Phe
305 310 315 320

Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val Ala
325 330 335

Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala Asn

340

345

350

Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg Val
 355 360 365

Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly Ile
 370 375 380

Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His Leu
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Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr
 405 410

<210> 13

<211> 365

<212> PRT

<213> human

<400> 13

Met Asp Ile Ile Glu Thr Ala Lys Leu Glu Glu His Lys Glu Asn Gln
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 20 25 30

Glu Glu Asn Lys Asn Gly Asn Gly Lys Pro Lys Ser Leu Ser Ser Gly
 35 40 45

Leu Arg Lys Gly Thr Lys Lys Tyr Pro Asp Tyr Ile Gln Ile Ala Met
 50 55 60

Pro Thr Glu Ser Arg Asn Lys Phe Pro Leu Glu Trp Trp Lys Thr Gly
 65 70 75 80

Ile Ala Phe Ile Tyr Ala Val Phe Asn Leu Val Leu Thr Thr Val Met
 85 90 95

Ile Thr Val Val His Glu Arg Val Pro Pro Lys Glu Leu Ser Pro Pro
 100 105 110

Leu Pro Asp Lys Phe Phe Asp Tyr Ile Asp Arg Val Lys Trp Ala Phe
 115 120 125

Ser Val Ser Glu Ile Asn Gly Ile Ile Leu Val Gly Leu Trp Ile Thr		
130	135	140
Gln Trp Leu Phe Leu Arg Tyr Lys Ser Ile Val Gly Arg Arg Phe Cys		
145	150	155 160
Phe Ile Ile Gly Thr Leu Tyr Leu Tyr Arg Cys Ile Thr Met Tyr Val		
	165	170 175
Thr Thr Leu Pro Val Pro Gly Met His Phe Gln Cys Ala Pro Lys Leu		
	180	185 190
Asn Gly Asp Ser Gln Ala Lys Val Gln Arg Ile Leu Arg Leu Ile Ser		
	195	200 205
Gly Gly Gly Leu Ser Ile Thr Gly Ser His Ile Leu Cys Gly Asp Phe		
	210	215 220
Leu Phe Ser Gly His Thr Val Thr Leu Thr Leu Thr Tyr Leu Phe Ile		
225	230	235 240
Lys Glu Tyr Ser Pro Arg His Phe Trp Trp Tyr His Leu Ile Cys Trp		
	245	250 255
Leu Leu Ser Ala Ala Gly Ile Ile Cys Ile Leu Val Ala His Glu His		
	260	265 270
Tyr Thr Ile Asp Val Ile Ile Ala Tyr Tyr Ile Thr Thr Arg Leu Phe		
	275	280 285
Trp Trp Tyr His Ser Met Ala Asn Glu Lys Asn Leu Lys Val Ser Ser		
	290	295 300
Gln Thr Asn Phe Leu Ser Arg Ala Trp Trp Phe Pro Ile Phe Tyr Phe		
305	310	315 320
Phe Glu Lys Asn Val Gln Gly Ser Ile Pro Cys Cys Phe Ser Trp Pro		
	325	330 335
Leu Ser Trp Pro Pro Gly Cys Phe Lys Ser Ser Cys Lys Lys Thr Ser		
	340	345 350

Arg Val Gln Lys Ile Gly Glu Asp Asn Glu Leu Ser Thr
355 360 365

<210> 14
<211> 451
<212> PRT
<213> C. elegans

<400> 14

Met Lys Met Ser Trp Asn His Gln Tyr Thr Asn Tyr Gly Ser Ile Ala
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Asp Asp Asn Gly Asp Glu Glu Lys Ala Glu Asn Ser Glu Gly Ala Ala
20 25 30

Ala Glu Lys Val Glu Lys Gln His Asp Asp Asp Gly Val Val Val His
35 40 45

Glu Glu Thr Asp Gly Val Ala Ser Ser Arg Ser Ser His His Asp Lys
50 55 60

Gln Lys Pro Gly Glu Thr Lys Lys Ser Gly Asp Gly Lys Met Asp Asp
65 70 75 80

Asp Asp Ile Ile Thr Thr Ala Arg Ser Ser Ser Ser Arg Arg Ile Cys
85 90 95

Gly Ser Ala Ala Ser Ser Ser Asp Ser Glu Thr Ala Asp Asp Ala Pro
100 105 110

Leu Leu Pro Asp Glu Gly Pro Ser His Ala Val Arg Leu Glu Met Pro
115 120 125

Gly Asp Lys Pro Ala Ser Pro His Asp Arg Phe Pro Lys Thr Pro Leu
130 135 140

Lys Thr Leu Val Ala Phe Leu Met Leu Val Val Ala Ala Ala Gly Asn
145 150 155 160

Thr Ile Thr Leu Ser Trp Ile His Glu Arg Tyr Pro Leu Thr Pro Pro
165 170 175

Leu Pro Asp Ile Val Phe Glu Leu Ile Pro Lys Ile Pro Trp Gly Leu
180 185 190

Arg Leu Cys Glu Asn Leu Met Ile Gly Ser Phe Val Ser Leu Leu Val
195 200 205

Leu Ile Leu Phe His Arg His Arg Trp Ile Val Leu Arg Arg Leu Cys
210 215 220

Phe Ile Gly Ser Ile Leu Tyr Gly Met Arg Cys Ile Thr Met Met Val
225 230 235 240

Thr Pro Val Pro Lys Ala Asp Glu Asp Phe Glu Cys Ser Pro Arg Phe
245 250 255

Gly Glu Asn Ala Thr Phe Ser Leu Ile Val Met Arg Gly Val Trp Ser
260 265 270

Met Phe Gly Leu Gly Leu Asn Leu Phe Asp Asn Gln Lys Val Val Leu
275 280 285

Cys Gly Asp Tyr Ile Tyr Ser Gly His Thr Leu Val Leu Val Val Ser
290 295 300

Ala Leu Phe Ile Gly Glu Tyr Ser Pro Arg Arg Phe Tyr Ile Leu His
305 310 315 320

Trp Leu Ser Trp Leu Val Cys Ser Val Gly Val Ile Phe Leu Val Leu
325 330 335

Ser His Gly His Tyr Thr Ile Asp Val Ile Leu Ser Tyr Phe Ala Cys
340 345 350

Thr Arg Val Phe Trp Ala Tyr His Thr Gln Ala Ala His Pro Ser Ile
355 360 365

Arg Leu Ser Val Gln Asn His Gln Ala Lys Glu Phe Trp Phe Pro Leu
370 375 380

Leu Arg Trp Phe Glu Gly Asp Ile Arg Arg Pro Val Pro Arg Arg Phe
385 390 395 400

Asp Cys Pro Ile Ser Tyr Ser Gln Thr Pro Val Asp Tyr Ser Phe Leu
405 410 415

Pro Trp Phe Ser Phe Phe Phe Gln Ser Asn Pro Met Met Phe Pro Gly
420 425 430

Ala Phe Thr Phe Tyr His Thr Gln Asn His Ser Lys Ser Thr Met Ser
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Leu Pro Lys
450

<210> 15
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<212> PRT
<213> C. elegans

<400> 15

Met Thr Asn Ser Ser Glu Phe Thr Asp Val Leu Gln Ser Arg Asp Pro
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Cys Val Ser Asn Gly Ile Val Ile Asn Ile Asp Pro Ile Asp Pro Glu
20 25 30

Pro Thr Pro Ile Arg Lys Glu Phe Thr Cys Glu Asp Thr Phe His His
35 40 45

Glu His His Gly Asn Ser Glu Gly Phe Lys Thr Leu Thr Ala Phe Leu
50 55 60

Cys Leu Met Leu Ser Ala Phe Leu Asn Phe Phe Leu Leu Thr Val Ile
65 70 75 80

His Asp Val Val Pro Arg Gln Pro Leu Pro Asp Leu Thr Phe Met Ile
85 90 95

Ile Pro Gln Gln Arg Trp Ala Trp Ser Val Gly Asp Val Leu Ser Thr
100 105 110

Val Ser Ser Val Val Ala Phe Thr Ile Ile Phe Leu His His Gln Arg
115 120 125

Trp Ile Val Leu Arg Arg Thr Phe Leu Leu Gly Ala Ile Met Tyr Gly
130 135 140

Leu Arg Ala Val Ile Leu Gly Val Thr Phe Leu Pro Pro Ser Phe His

145 150 155 160

Asn Arg Asp Glu Ile Cys Gln Pro Gln Val Asn Arg Thr Ala Met Tyr
 165 170 175

Gly Met Glu Ile Ala Thr Arg Phe Leu Thr Tyr Val Ile Thr Leu Gly
 180 185 190

Leu Thr Ser Gly Gln Asp Lys Ile Leu Cys Gly Asp Leu Met Phe Ser
 195 200 205

Gly His Thr Val Val Leu Thr Ile Met Tyr Phe Val Gln Leu Gln Tyr
 210 215 220

Thr Pro Arg Gly Leu Val Ile Leu Arg Tyr Ile Ala Ala Pro Ile Thr
225 230 235 240

Phe Leu Gly Ile Ala Ala Leu Val Val Ser Gly Gly His Tyr Thr Met
 245 250 255

Asp Val Leu Ile Ala Tyr Trp Leu Thr Ser His Val Phe Trp Ser Tyr
 260 265 270

His Gln Ile Phe Glu Met Arg Lys Asp Asp Arg Pro Gln Ala Pro Leu
 275 280 285

Ser Arg Leu Trp Trp Phe Trp Leu Cys Tyr Trp Phe Glu Ser Asp Val
 290 295 300

Ala Asp Gly Lys Leu Val Asn Lys Trp Asn Trp Pro Leu Glu Gly Pro
305 310 315 320

Gln Arg Met His Thr Ile Met Asn Arg Ile Asn Tyr Lys Leu Gln
 325 330 335

<210> 16
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<212> PRT
<213> C. elegans

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Met Gly Ser Val Ser Lys Thr Val Ile Ser Ala Arg Gly Ala Ser Pro
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Asp Asp Glu Gln Asn Gly Thr Lys Asn Gly Ile Ser Asn Gly Ser Glu
20 25 30

Trp Ala Lys Cys Ile Phe Leu Phe Phe Phe Leu Phe Ile Ala Gly Met
35 40 45

Ser Asn Trp Ala Val Leu Ala Tyr Thr His Asp Tyr Val Pro Arg Glu
50 55 60

Ser Leu Pro Asp Ile Val Phe Ser Leu Val Ser Glu Gln Arg Trp Ala
65 70 75 80

Ser Ser Leu Gly Asp Phe Cys Val Ala Leu Cys Ile Val Met Leu Gly
85 90 95

Ala Leu Leu Val Ile His Gln His Arg Gly Thr Ile Leu Lys Arg Val
100 105 110

Val Phe Cys Ala Gly Thr Leu Tyr Ala Met Arg Ser Val Thr Leu Ala
115 120 125

Ala Thr Gln Leu Pro Ser Gly Tyr Thr Asp Asn Gln Gly Arg Cys Arg
130 135 140

Asp Gln Val Glu Ser Glu Ala Gly Val Phe Phe Gly Arg Leu Phe Glu
145 150 155 160